AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph at page 25, starting at line 8 as follows:

In general, a nucleic acid molecule that hybridizes to a recited sequence under moderately stringent conditions will have greater than about 60% identity, such as greater than about 70% identity or greater than about 80% identity to the reference sequence over the length of the two sequences being compared. A nucleic acid molecule that hybridizes to a recited sequence under highly stringent conditions will generally have greater than about 90% identity, including greater than about 95% identity, to the reference sequence over the length of the two sequences being compared. Identity of any two nucleic acid sequences can be determined by those skilled in the art based, for example, on a BLAST 2.0 computer alignment, using default parameters. BLAST 2.0 searching is available on the world wide web at http://www.ncbi.nlm.nih.gov/gorf/bl2.html., as described by Tatiana et al., FEMS Microbiol Lett. 174:247-250 (1999).

Please amend the paragraph at page 26, starting at line 17 as follows:

It is understood that a Nope nucleic acid molecule, as used herein, specifically excludes previously known nucleic acid molecules consisting of nucleotide sequences having identity with the Nope nucleotide sequence (SEQ ID NO:1), such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites (STSs) and genomic fragments, deposited in public databases such as the nr, dbest, dbsts, gss and htgs databases, which are available for searching on the world wide web at http://www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=0, using the program BLASTN 2.0.9 described by Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997).